RAW SEQUENCE LISTING   DATE: 11/05/2001
PATENT APPLICATION: US/09/508,832   TIME: 13:20:14

Input Set : A:\17227159.app
Output Set: N:\CRF3\11022001\I508832.raw

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 3 <110> APPLICANT: CORY, SUZANNE
 4       ADAMS, JERRY
 5       HUANG, DAVID C.S.
 6       O'CONNOR, LIAM
 7       STRASSER, ANDREAS
 8       PUTHALAKATH, HAMSA
 9       O'REILLY, LORRAINE
11 <120> TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES
13 <130> FILE REFERENCE: 017227/0159
15 <140> CURRENT APPLICATION NUMBER: 09/508,832
16 <141> CURRENT FILING DATE: 2000-07-10
18 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00772
19 <151> PRIOR FILING DATE: 1998-09-17
21 <150> PRIOR APPLICATION NUMBER: AU PO 9263
22 <151> PRIOR FILING DATE: 1997-09-17
24 <150> PRIOR APPLICATION NUMBER: AU PO 9373
25 <151> PRIOR FILING DATE: 1997-09-24
27 <160> NUMBER OF SEQ ID NOS: 39
29 <170> SOFTWARE: PatentIn Ver. 2.1
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46 Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
47                20                  25                  30
49 cct acc tcc cta cag aca gaa ccg caa gct tcc ata cga cag tct cag    144
50 Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
51             35                  40                  45
53 gag gaa cct gaa gat ctg cgc ccg gag ata cgg att gca cag gag ctg    192
54 Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
55         50                  55                  60
57 cgg cgg atc gga gac gag ttc aac gaa act tac aca agg agg gtg ttt    240
58 Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
59  65                  70                  75                  80
61 gca aat gat tac cgc gag gct gaa gac cac cct caa atg gtt atc tta    288
62 Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
63                 85                  90                  95
65 caa ctg tta cgc ttt atc ttc cgt ctg gta tgg aga agg cat tg        332
66 Gln Leu Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
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80              20                  25                  30
82 Pro Thr Ser Leu Gln Thr Glu Pro Gln Ala Ser Ile Arg Gln Ser Gln
83              35                  40                  45
85 Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu
86       50                  55                  60
88 Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe
89  65                  70                  75                  80
91 Ala Asn Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu
92              85                  90                  95
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95              100                105                110
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99 <211> LENGTH: 422
100 <212> TYPE: DNA
101 <213> ORGANISM: Mus sp.
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105 <222> LOCATION: (1)..(420)
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110  1               5                   10                  15
112 gga caa ttg cag cct gct gag agg cct ccc cag ctc agg cct ggg gcc    96
113 Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
114              20                  25                  30
116 cct acc tcc cta cag aca gaa ccg caa gac agg agc ccg gca ccc atg   144
117 Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
118              35                  40                  45
120 agt tgt gac aag tca aca caa acc cca agt cct cct tgc cag gcc ttc   192
121 Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
122       50                  55                  60
124 aac cac tat ctc agt gca atg gct tcc ata cga cag tct cag gag gaa   240
125 Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu
126  65                  70                  75                  80
128 cct gaa gat ctg cgc ccg gag ata cgg att gca cag gag ctg cgg cgg   288
129 Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg
130              85                  90                  95
132 atc gga gac gag ttc aac gaa act tac aca agg agg gtg ttt gca aat   336
133 Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn
134              100                105                110
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137 Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu
138         115                 120                 125
140 tta cgc ttt atc ttc cgt ctg gta tgg aga agg cat tg                 422
141 Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
142     130                 135                 140
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146 <211> LENGTH: 140
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148 <213> ORGANISM: Mus sp.
150 <400> SEQUENCE: 4
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152   1                 5                 10                 15
154 Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
155             20                 25                 30
157 Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
158         35                 40                 45
160 Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
161     50                 55                 60
163 Asn His Tyr Leu Ser Ala Met Ala Ser Ile Arg Gln Ser Gln Glu Glu
164  65                 70                 75                 80
166 Pro Glu Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg
167             85                 90                 95
169 Ile Gly Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg Val Phe Ala Asn
170             100                 105                 110
172 Asp Tyr Arg Glu Ala Glu Asp His Pro Gln Met Val Ile Leu Gln Leu
173         115                 120                 125
175 Leu Arg Phe Ile Phe Arg Leu Val Trp Arg Arg His
176     130                 135                 140
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180 <211> LENGTH: 590
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186 <222> LOCATION: (1)..(588)
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191   1                 5                 10                 15
193 gga caa ttg cag cct gct gag agg cct ccc cag ctc agg cct ggg gcc     96
194 Gly Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
195             20                 25                 30
197 cct acc tcc cta cag aca gaa ccg caa ggt aat ccc gac ggc gaa ggg    144
198 Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
199         35                 40                 45
201 gac cgc tgc ccc cac ggc agc cct cag ggc ccg ctg gcc cca ccg gcc    192
202 Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
203     50                 55                 60
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205 agc cct ggc cct ttt gct acc aga tcc cca ctt ttc atc ttt gtg aga    240
206 Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
207 65                  70                  75                  80
209 aga tct tct ctg ctg tcc cgg tcc tcc agt ggg tat ttc tct ttt gac    288
210 Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
211                 85                  90                  95
213 aca gac agg agc ccg gca ccc atg agt tgt gac aag tca aca caa acc    336
214 Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
215                 100                 105                 110
217 cca agt cct cct tgc cag gcc ttc aac cac tat ctc agt gca atg gct    384
218 Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
219         115                 120                 125
221 tcc ata cga cag tct cag gag gaa cct gaa gat ctg cgc ccg gag ata    432
222 Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
223         130                 135                 140
225 cgg att gca cag gag ctg cgg cgg atc gga gac gag ttc aac gaa act    480
226 Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Glu Thr
227 145                 150                 155                 160
229 tac aca agg agg gtg ttt gca aat gat tac cgc gag gct gaa gac cac    528
230 Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
231                 165                 170                 175
233 cct caa atg gtt atc tta caa ctg tta cgc ttt atc ttc cgt ctg gta    576
234 Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
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238 Trp Arg Arg His
239         195
242 <210> SEQ ID NO: 6
243 <211> LENGTH: 196
244 <212> TYPE: PRT
245 <213> ORGANISM: Mus sp.
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252                 20                  25                  30
254 Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Asp Gly Glu Gly
255         35                  40                  45
257 Asp Arg Cys Pro His Gly Ser Pro Gln Gly Pro Leu Ala Pro Pro Ala
258         50                  55                  60
260 Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile Phe Val Arg
261 65                  70                  75                  80
263 Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr Phe Ser Phe Asp
264                 85                  90                  95
266 Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys Ser Thr Gln Thr
267                 100                 105                 110
269 Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu Ser Ala Met Ala
270         115                 120                 125
272 Ser Ile Arg Gln Ser Gln Glu Glu Pro Glu Asp Leu Arg Pro Glu Ile
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Input Set : A:\17227159.app
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273      130                  135                  140
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276 145                  150                  155                  160
278 Tyr Thr Arg Arg Val Phe Ala Asn Asp Tyr Arg Glu Ala Glu Asp His
279                  165                  170                  175
281 Pro Gln Met Val Ile Leu Gln Leu Leu Arg Phe Ile Phe Arg Leu Val
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284 Trp Arg Arg His
285          195
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289 <211> LENGTH: 416
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291 <213> ORGANISM: Homo sapiens
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303 Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
304              20                  25                  30
306 cct acc tcc cta cag aca gag cca caa gac agg agc cca gca ccc atg   144
307 Pro Thr Ser Leu Gln Thr Glu Pro Gln Asp Arg Ser Pro Ala Pro Met
308          35                  40                  45
310 agt tgt gac aaa tca aca caa acc cca agt cct cct tgc cag gcc ttc   192
311 Ser Cys Asp Lys Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe
312          50                  55                  60
314 aac cac tat ctc agt gca atg gct tcc atg agg cag gct gaa cct gca   240
315 Asn His Tyr Leu Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala
316  65                  70                  75                  80
318 gat atg cgc cca gag ata tgg atc gcc caa gag ttg cgg cgt atc gga   288
319 Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly
320              85                  90                  95
322 gac gag ttt aac gct tac tat gca agg agg gta ttt ttg aat aat tac   336
323 Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr
324          100                  105                  110
326 caa gca gcc gaa gac cac cca cga atg gtt atc tta cga ctg tta cgt   384
327 Gln Ala Ala Glu Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg
328          115                  120                  125
330 tac att gtc cgc ctg gtg tgg aga atg cat tg                        416
331 Tyr Ile Val Arg Leu Val Trp Arg Met His
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335 <210> SEQ ID NO: 8
336 <211> LENGTH: 138
337 <212> TYPE: PRT
338 <213> ORGANISM: Homo sapiens
340 <400> SEQUENCE: 8
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VERIFICATION SUMMARY   DATE: 11/05/2001
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Input Set : **A:\17227159.app**
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